



# 15  
12/28/94

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of  
Thomas R. Adams et al.

Serial No. 08/113,561

Filed: August 25, 1993

For: METHODS AND COMPOSITIONS  
FOR THE PRODUCTION OF  
STABLY TRANSFORMED,  
FERTILE MONOCOT PLANTS  
AND CELLS THEREOF

§  
§  
§ Group Art Unit: 1804  
§  
§ Examiner: G. Benzion  
§  
§ Atty. Dkt.: DEKM:055/PAR  
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§  
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§  
§  
§

CERTIFICATE OF MAILING  
37 C.F.R. 1.8

I hereby certify that this correspondence is being deposited  
with the U.S. Postal Service as First Class Mail in an  
envelope addressed to: Commissioner of Patents and  
Trademarks, Washington, D.C. 20541, on the date below:

December 8, 1994

Date

David L. Parker

**STATEMENT AS REQUIRED UNDER 37 C.F.R. § 1.825(a) and (b)  
AND STATEMENT AS REQUIRED UNDER 37 C.F.R. § 1.821(q)**

ATTN: BOX SEQUENCE  
Honorable Commissioner of  
Patents and Trademarks  
Washington, D.C. 20231

Sir:

Submitted herewith is a substitute computer readable form  
and a substitute paper copy of the sequence listing of those  
sequences in the captioned patent application, wherein minor  
errors have been corrected. The substitute computer readable  
form of the sequence listing is the same as the substitute paper  
copy of the sequence listing. The sequence information provided

in the Specification is also the same as the sequence listing of the enclosed substitute computer readable and paper forms of the sequence listing.

In accordance with 37 C.F.R. § 1.821(g), it is herewith represented that no new matter is included with this submission.

  
Respectfully submitted,

David L. Parker  
Reg. No. 32,165

ARNOLD, WHITE & DURKEE  
P. O. Box 4433  
Houston, Texas 77210  
(512) 320-7200

Date: December 8, 1994

*h:\dekm\055\pa\state.2*

## SEQUENCE LISTING

### (1) GENERAL INFORMATION:

- (i) APPLICANT: Adams, Thomas R. et al.
- (ii) TITLE OF INVENTION: Methods and Compositions for the Production of Stably Transformed, Fertile Monocot Plants and Cells Thereof
- (iii) NUMBER OF SEQUENCES: 26
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Arnold, White & Durkee
  - (B) STREET: P.O. Box 4433
  - (C) CITY: Houston
  - (D) STATE: Texas
  - (E) COUNTRY: USA
  - (F) ZIP: 77210
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/113,561
  - (B) FILING DATE: 25-AUG-1993
  - (C) CLASSIFICATION: Unknown
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 07/565,844
  - (B) FILING DATE: 09-AUG-1990
  - (C) CLASSIFICATION: Unknown
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Parker, David L.
  - (B) REGISTRATION NUMBER: 32,165
  - (C) REFERENCE/DOCKET NUMBER: DEKM:055/PAR
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 512/418-3000
  - (B) TELEFAX: 713/789-2679
  - (C) TELEX: 79-0924

### (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 amino acid residues
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Ala Thr Val Pro Glu Leu Asn Cys Glu Met Pro Pro Ser Asp

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAGGATCCGT CGACATGGTA AGCTTAGCGG GCCCC

35

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GATCCGTCGA CCATGGCGCT TCAAGCTTC

29

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCAGCTGGTA CCGCGAAGTT CGAAGGGCT

29

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTAGACAACA AAGCAGCAAC CATGGCCAGC ATGCAAGGCC TCATGCATC

49

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCGGGATGCA TGAGGCCTTG CATGCTGGCC ATGGTTGCTG CTTTGTGTGT

49

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acid residues
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Ala	Ser	Met	Gln	Gly	Leu	Met	His	Pro	Gly
1				5					10	

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acid residues
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Val	Lys	Cys	Met	Gln	Val
1				5	

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AAGUGAAGUG AAGUGAAG

18

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1845 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 1..1839

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATC	GAA	AAC	AAT	CCG	AAC	ATC	AAT	GAA	TGC	ATT	CCT	TAC	AAT	TGC	CTC	48
Met	Asp	Asn	Asn	Pro	Asn	Ile	Asn	Glu	Cys	Ile	Pro	Tyr	Asn	Cys	Leu	
1				5				10						15		
AGC	AAC	CCT	GAA	GTG	GAA	GTG	CTG	GGT	GGC	GAA	CGC	ATC	GAA	ACC	GGT	96
Ser	Asn	Pro	Glu	Val	Glu	Val	Leu	Gly	Gly	Glu	Arg	Ile	Glu	Thr	Gly	
			20					25						30		
TAC	ACC	CCA	ATC	GAT	ATT	TCC	CTG	TCC	CTG	ACC	CAA	TTT	CTG	CTG	AGC	144
Tyr	Thr	Pro	Ile	Asp	Ile	Ser	Leu	Ser	Leu	Thr	Gln	Phe	Leu	Leu	Ser	
		35					40					45				
GAA	TTT	GTG	CCC	GGT	GCT	GGC	TTT	GTG	CTG	GGC	CTG	GTG	GAT	ATC	ATC	192
Glu	Phe	Val	Pro	Gly	Ala	Gly	Phe	Val	Leu	Gly	Leu	Val	Asp	Ile	Ile	
	50					55					60					
TGG	GGC	ATT	TTT	GGT	CCC	TCC	CAA	TGG	GAC	GCC	TTT	CTG	GTG	CAA	ATT	240
Trp	Gly	Ile	Phe	Gly	Pro	Ser	Gln	Trp	Asp	Ala	Phe	Leu	Val	Gln	Ile	
65					70				75						80	
GAA	CAG	CTG	ATT	AAC	CAA	CGC	ATC	GAA	GAA	TTC	GCT	AGG	AAC	CAA	GCC	288
Glu	Gln	Leu	Ile	Asn	Gln	Arg	Ile	Glu	Glu	Phe	Ala	Arg	Asn	Gln	Ala	
				85					90					95		
ATT	TCC	CGC	CTG	GAA	GGC	CTG	AGC	AAT	CTG	TAC	CAA	ATT	TAC	GCC	GAA	336
Ile	Ser	Arg	Leu	Glu	Gly	Leu	Ser	Asn	Leu	Tyr	Gln	Ile	Tyr	Ala	Glu	
			100					105					110			
TCC	TTT	CGC	GAG	TGG	GAA	GCC	GAT	CCT	ACC	AAT	CCA	GCC	CTG	CGC	GAA	384
Ser	Phe	Arg	Glu	Trp	Glu	Ala	Asp	Pro	Thr	Asn	Pro	Ala	Leu	Arg	Glu	
		115					120					125				
GAG	ATG	CGC	ATT	CAA	TTC	AAT	GAC	ATG	AAC	AGC	GCC	CTG	ACC	ACC	GCT	432
Glu	Met	Arg	Ile	Gln	Phe	Asn	Asp	Met	Asn	Ser	Ala	Leu	Thr	Thr	Ala	
	130					135					140					
ATT	CCT	CTG	TTT	GCC	GTG	CAA	AAT	TAC	CAA	GTG	CCT	CTG	CTG	TCC	GTG	480
Ile	Pro	Leu	Phe	Ala	Val	Gln	Asn	Tyr	Gln	Val	Pro	Leu	Leu	Ser	Val	
145					150				155						160	
TAC	GTG	CAA	GCT	GCC	AAT	CTG	CAT	CTG	TCC	GTG	CTG	CGC	GAT	GTG	TCC	528
Tyr	Val	Gln	Ala	Ala	Asn	Leu	His	Leu	Ser	Val	Leu	Arg	Asp	Val	Ser	
			165					170						175		
GTG	TTT	GGC	CAA	AGG	TGG	GGC	TTT	GAT	GCC	GCC	ACC	ATC	AAT	AGC	CGC	576
Val	Phe	Gly	Gln	Arg	Trp	Gly	Phe	Asp	Ala	Ala	Thr	Ile	Asn	Ser	Arg	
			180					185					190			
TAC	AAT	GAT	CTG	ACC	AGG	CTG	ATT	GGC	AAC	TAC	ACC	GAT	TAC	GCT	GTG	624
Tyr	Asn	Asp	Leu	Thr	Arg	Leu	Ile	Gly	Asn	Tyr	Thr	Asp	Tyr	Ala	Val	
		195					200					205				
CGC	TGG	TAC	AAT	ACC	GGC	CTG	GAA	CGC	GTG	TGG	GGC	CCA	GAT	TCC	CGC	672
Arg	Trp	Tyr	Asn	Thr	Gly	Leu	Glu	Arg	Val	Trp	Gly	Pro	Asp	Ser	Arg	
	210					215					220					

GAT Asp 225	TGG Trp	GTG Val	AGG Arg	TAC Tyr	AAT Asn 230	CAA Gln	TTT Phe	CGC Arg	CGC Arg	GAA Glu 235	CTG Leu	ACC Thr	CTG Leu	ACC Thr	GTG Val 240	720
CTC Leu	GAT Asp	ATC Ile	GTG Val	GCT Ala 245	CTG Leu	TTC Phe	CCA Pro	AAT Asn	TAC Tyr 250	GAT Asp	AGC Ser	CGC Arg	CGC Arg	TAC Tyr 255	CCA Pro	768
ATT Ile	CGA Arg	ACC Thr	GTG Val 260	TCC Ser	CAA Gln	CTG Leu	ACC Thr	CGC Arg 265	GAA Glu	ATT Ile	TAC Tyr	ACC Thr	AAC Asn 270	CCA Pro	GTG Val	816
CTG Leu	GAA Glu	AAT Asn 275	TTT Phe	GAT Asp	GGT Gly	AGC Ser	TTT Phe 280	CGC Arg	GGC Gly	TCC Ser	GCT Ala	CAG Gln 285	GGC Gly	ATC Ile	GAA Glu	864
CGC Arg	AGC Ser 290	ATT Ile	AGG Arg	AGC Ser	CCA Pro	CAT His 295	CTG Leu	ATG Met	GAT Asp	ATC Ile	CTG Leu 300	AAC Asn	AGC Ser	ATC Ile	ACC Thr	912
ATC Ile 305	TAC Tyr	ACC Thr	GAT Asp	GCT Ala	CAT His 310	AGG Arg	GGT Gly	TAC Tyr	TAC Tyr	TAC Tyr 315	TGG Trp	TCC Ser	GGC Gly	CAT His	CAA Gln 320	960
ATC Ile	ATG Met	GCT Ala	TCC Ser	CCT Pro 325	GTG Val	GGC Gly	TTT Phe	TCC Ser	GGG Gly 330	CCA Pro	GAA Glu	TTC Phe	ACC Thr	TTT Phe 335	CCA Pro	1008
CTG Leu	TAC Tyr	GGC Gly	ACG Thr 340	ATG Met	GGC Gly	AAT Asn	GCC Ala	GCT Ala 345	CCA Pro	CAA Gln	CAA Gln	CGC Arg	ATT Ile 350	GTG Val	GCT Ala	1056
CAA Gln	CTG Leu	GGT Gly 355	CAG Gln	GGC Gly	GTG Val	TAC Tyr	CGC Arg 360	ACC Thr	CTG Leu	TCC Ser	TCC Ser	ACC Thr 365	CTG Leu	TAC Tyr	CGC Arg	1104
CGC Arg	CCT Pro 370	TTT Phe	AAT Asn	ATC Ile	GGC Gly	ATC Ile 375	AAC Asn	AAC Asn	CAG Gln	CAA Gln 380	CTG Leu	TCC Ser	GTG Val	CTG Leu	GAC Asp	1152
GGC Gly 385	ACC Thr	GAA Glu	TTT Phe	GCT Ala	TAC Tyr 390	GGC Gly	ACC Thr	TCC Ser	TCC Ser	AAT Asn 395	CTG Leu	CCA Pro	TCC Ser	GCT Ala	GTA Val 400	1200
TAC Tyr	CGC Arg	AAG Lys	AGC Ser	GGC Gly 405	ACC Thr	GTG Val	GAT Asp	TCC Ser	CTG Leu 410	GAT Asp	GAA Glu	ATC Ile	CCA Pro	CCA Pro	CAG Gln 415	1248
AAT Asn	AAC Asn	AAC Asn	GTG Val 420	CCA Pro	CCT Pro	AGG Arg	CAA Gln	GGC Gly 425	TTT Phe	AGC Ser	CAT His	CGC Arg	CTG Leu 430	AGC Ser	CAT His	1296
GTG Val	TCC Ser	ATG Met 435	TTT Phe	CGC Arg	TCC Ser	GGC Gly	TTT Phe 440	AGC Ser	AAT Asn	AGC Ser	AGC Ser	GTG Val 445	AGC Ser	ATC Ile	ATC Ile	1344
CGC Arg	GCT Ala 450	CCT Pro	ATG Met	TTC Phe	TCC Ser	TGG Trp 455	ATC Ile	CAT His	CGC Arg	AGC Ser	GCT Ala 460	GAA Glu	TTT Phe	AAC Asn	AAC Asn	1392

ATC Ile 465	ATT Ile	GCC Ala	TCC Ser	GAT Asp	AGC Ser 470	ATT Ile	ACC Thr	CAA Gln	ATC Ile	CCT Pro 475	GCC Ala	GTG Val	AAG Lys	GGC Gly 480	AAC Asn	1440
TTT Phe	CTG Leu	TTT Phe	AAT Asn 485	GGT Gly	TCC Ser	GTG Val	ATT Ile	TCC Ser	GGC Gly 490	CCA Pro	GGC Gly	TTT Phe	ACC Thr	GGT Gly 495	GGC Gly	1488
GAC Asp	CTG Leu	GTG Val	CGC Arg 500	CTG Leu	AAT Asn	AGC Ser	AGC Ser	GGC Gly 505	AAT Asn	AAC Asn	ATT Ile	CAG Gln	AAT Asn 510	CGC Arg	GGC Gly	1536
TAC Tyr	ATT Ile	GAA Glu 515	GTG Val	CCA Pro	ATT Ile	CAC His	TTC Phe 520	CCA Pro	TCC Ser	ACC Thr	TCC Ser	ACC Thr 525	CGC Arg	TAC Tyr	CGC Arg	1584
GTG Val 530	CGC Arg	GTG Val	CGC Arg	TAC Tyr	GCT Ala	TCC Ser 535	GTG Val	ACC Thr	CCA Pro	ATT Ile	CAC His 540	CTC Leu	AAC Asn	GTT Val	AAC Asn	1632
TGG Trp 545	GGC Gly	AAT Asn	TCC Ser	TCC Ser	ATT Ile 550	TTT Phe	TCC Ser	AAT Asn	ACC Thr	GTG Val 555	CCA Pro	GCT Ala	ACC Thr	GCT Ala 560	ACC Thr	1680
TCC Ser	CTG Leu	GAT Asp	AAT Asn 565	CTG Leu	CAA Gln	TCC Ser	AGC Ser	GAT Asp 570	TTT Phe	GGT Gly	TAC Tyr	TTT Phe	GAA Glu 575	AGC Ser	GCC Ala	1728
AAT Asn	GCT Ala	TTT Phe	ACC Thr 580	TCC Ser	TCC Ser	CTG Leu	GGT Gly 585	AAT Asn	ATC Ile	GTG Val	GGT Gly	GTG Val	CGC Arg 590	AAT Asn	TTT Phe	1776
AGC Ser	GGC Gly	ACC Thr 595	GCC Ala	GGC Gly	GTG Val	ATC Ile	ATC Ile 600	GAC Asp	CGC Arg	TTT Phe	GAA Glu 605	TTT Phe	ATT Ile	CCA Pro	GTG Val	1824
ACC Thr 610	GCC Ala	ACC Thr	CTC Leu	GAG Glu	TAGGTA											1845

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 613 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met 1	Asp	Asn	Asn	Pro 5	Asn	Ile	Asn	Glu	Cys 10	Ile	Pro	Tyr	Asn	Cys 15	Leu
Ser	Asn	Pro	Glu 20	Val	Glu	Val	Leu	Gly 25	Gly	Glu	Arg	Ile	Glu 30	Thr	Gly
Tyr	Thr	Pro	Ile	Asp	Ile	Ser	Leu	Ser	Leu	Thr	Gln	Phe	Leu	Leu	Ser



Glu	Phe	Val	Pro	Gly	Ala	Gly	Phe	Val	Leu	Gly	Leu	Val	Asp	Ile	Ile
	50					55					60				
Trp	Gly	Ile	Phe	Gly	Pro	Ser	Gln	Trp	Asp	Ala	Phe	Leu	Val	Gln	Ile
65					70					75					80
Glu	Gln	Leu	Ile	Asn	Gln	Arg	Ile	Glu	Glu	Phe	Ala	Arg	Asn	Gln	Ala
				85					90					95	
Ile	Ser	Arg	Leu	Glu	Gly	Leu	Ser	Asn	Leu	Tyr	Gln	Ile	Tyr	Ala	Glu
			100					105					110		
Ser	Phe	Arg	Glu	Trp	Glu	Ala	Asp	Pro	Thr	Asn	Pro	Ala	Leu	Arg	Glu
		115					120					125			
Glu	Met	Arg	Ile	Gln	Phe	Asn	Asp	Met	Asn	Ser	Ala	Leu	Thr	Thr	Ala
	130					135					140				
Ile	Pro	Leu	Phe	Ala	Val	Gln	Asn	Tyr	Gln	Val	Pro	Leu	Leu	Ser	Val
145					150					155					160
Tyr	Val	Gln	Ala	Ala	Asn	Leu	His	Leu	Ser	Val	Leu	Arg	Asp	Val	Ser
				165					170					175	
Val	Phe	Gly	Gln	Arg	Trp	Gly	Phe	Asp	Ala	Ala	Thr	Ile	Asn	Ser	Arg
			180					185						190	
Tyr	Asn	Asp	Leu	Thr	Arg	Leu	Ile	Gly	Asn	Tyr	Thr	Asp	Tyr	Ala	Val
		195					200					205			
Arg	Trp	Tyr	Asn	Thr	Gly	Leu	Glu	Arg	Val	Trp	Gly	Pro	Asp	Ser	Arg
	210					215					220				
Asp	Trp	Val	Arg	Tyr	Asn	Gln	Phe	Arg	Arg	Glu	Leu	Thr	Leu	Thr	Val
225					230					235					240
Leu	Asp	Ile	Val	Ala	Leu	Phe	Pro	Asn	Tyr	Asp	Ser	Arg	Arg	Tyr	Pro
				245					250					255	
Ile	Arg	Thr	Val	Ser	Gln	Leu	Thr	Arg	Glu	Ile	Tyr	Thr	Asn	Pro	Val
			260					265						270	
Leu	Glu	Asn	Phe	Asp	Gly	Ser	Phe	Arg	Gly	Ser	Ala	Gln	Gly	Ile	Glu
		275					280					285			
Arg	Ser	Ile	Arg	Ser	Pro	His	Leu	Met	Asp	Ile	Leu	Asn	Ser	Ile	Thr
	290					295					300				
Ile	Tyr	Thr	Asp	Ala	His	Arg	Gly	Tyr	Tyr	Tyr	Trp	Ser	Gly	His	Gln
305					310					315					320
Ile	Met	Ala	Ser	Pro	Val	Gly	Phe	Ser	Gly	Pro	Glu	Phe	Thr	Phe	Pro
				325					330					335	
Leu	Tyr	Gly	Thr	Met	Gly	Asn	Ala	Ala	Pro	Gln	Gln	Arg	Ile	Val	Ala
			340					345					350		
Gln	Leu	Gly	Gln	Gly	Val	Tyr	Arg	Thr	Leu	Ser	Ser	Thr	Leu	Tyr	Arg

355

360

365

Arg	Pro	Phe	Asn	Ile	Gly	Ile	Asn	Asn	Gln	Gln	Leu	Ser	Val	Leu	Asp
370						375					380				
Gly	Thr	Glu	Phe	Ala	Tyr	Gly	Thr	Ser	Ser	Asn	Leu	Pro	Ser	Ala	Val
385					390					395					400
Tyr	Arg	Lys	Ser	Gly	Thr	Val	Asp	Ser	Leu	Asp	Glu	Ile	Pro	Pro	Gln
				405					410					415	
Asn	Asn	Asn	Val	Pro	Pro	Arg	Gln	Gly	Phe	Ser	His	Arg	Leu	Ser	His
			420					425					430		
Val	Ser	Met	Phe	Arg	Ser	Gly	Phe	Ser	Asn	Ser	Ser	Val	Ser	Ile	Ile
		435					440					445			
Arg	Ala	Pro	Met	Phe	Ser	Trp	Ile	His	Arg	Ser	Ala	Glu	Phe	Asn	Asn
	450					455					460				
Ile	Ile	Ala	Ser	Asp	Ser	Ile	Thr	Gln	Ile	Pro	Ala	Val	Lys	Gly	Asn
465					470					475					480
Phe	Leu	Phe	Asn	Gly	Ser	Val	Ile	Ser	Gly	Pro	Gly	Phe	Thr	Gly	Gly
				485					490					495	
Asp	Leu	Val	Arg	Leu	Asn	Ser	Ser	Gly	Asn	Asn	Ile	Gln	Asn	Arg	Gly
			500					505					510		
Tyr	Ile	Glu	Val	Pro	Ile	His	Phe	Pro	Ser	Thr	Ser	Thr	Arg	Tyr	Arg
		515					520					525			
Val	Arg	Val	Arg	Tyr	Ala	Ser	Val	Thr	Pro	Ile	His	Leu	Asn	Val	Asn
	530					535					540				
Trp	Gly	Asn	Ser	Ser	Ile	Phe	Ser	Asn	Thr	Val	Pro	Ala	Thr	Ala	Thr
545					550					555					560
Ser	Leu	Asp	Asn	Leu	Gln	Ser	Ser	Asp	Phe	Gly	Tyr	Phe	Glu	Ser	Ala
				565					570					575	
Asn	Ala	Phe	Thr	Ser	Ser	Leu	Gly	Asn	Ile	Val	Gly	Val	Arg	Asn	Phe
			580					585					590		
Ser	Gly	Thr	Ala	Gly	Val	Ile	Ile	Asp	Arg	Phe	Glu	Phe	Ile	Pro	Val
		595					600					605			
Thr	Ala	Thr	Leu	Glu											
610															

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1848 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1842

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATG	GAT	AAC	AAT	CCG	AAC	ATC	AAT	GAA	TGC	ATT	CCT	TAC	AAT	TGC	CTC	48
Met	Asp	Asn	Asn	Pro	Asn	Ile	Asn	Glu	Cys	Ile	Pro	Tyr	Asn	Cys	Leu	
1				5				10						15		
AGC	AAC	CCT	GAA	GTG	GAA	GTG	CTG	GGT	GGC	GAA	CGC	ATC	GAA	ACC	GGT	96
Ser	Asn	Pro	Glu	Val	Glu	Val	Leu	Gly	Gly	Glu	Arg	Ile	Glu	Thr	Gly	
			20					25					30			
TAC	ACC	CCA	ATC	GAT	ATT	TCC	CTG	TCC	CTG	ACC	CAA	TTT	CTG	CTG	AGC	144
Tyr	Thr	Pro	Ile	Asp	Ile	Ser	Leu	Ser	Leu	Thr	Gln	Phe	Leu	Leu	Ser	
		35					40					45				
GAA	TTT	GTG	CCC	GGT	GCT	GGC	TTT	GTG	CTG	GGC	CTG	GTG	GAT	ATC	ATC	192
Glu	Phe	Val	Pro	Gly	Ala	Gly	Phe	Val	Leu	Gly	Leu	Val	Asp	Ile	Ile	
	50					55					60					
TGG	GGC	ATT	TTT	GGT	CCC	TCC	CAA	TGG	GAC	GCC	TTT	CTG	GTG	CAA	ATT	240
Trp	Gly	Ile	Phe	Gly	Pro	Ser	Gln	Trp	Asp	Ala	Phe	Leu	Val	Gln	Ile	
65					70				75						80	
GAA	CAG	CTG	ATT	AAC	CAA	CGC	ATC	GAA	GAA	TTC	GCT	AGG	AAC	CAA	GCC	288
Glu	Gln	Leu	Ile	Asn	Gln	Arg	Ile	Glu	Glu	Phe	Ala	Arg	Asn	Gln	Ala	
				85					90					95		
ATT	TCC	CGC	CTG	GAA	GGC	CTG	AGC	AAT	CTG	TAC	CAA	ATT	TAC	GCC	GAA	336
Ile	Ser	Arg	Leu	Glu	Gly	Leu	Ser	Asn	Leu	Tyr	Gln	Ile	Tyr	Ala	Glu	
			100					105					110			
TCC	TTT	CGC	GAG	TGG	GAA	GCC	GAT	CCT	ACC	AAT	CCA	GCC	CTG	CGC	GAA	384
Ser	Phe	Arg	Glu	Trp	Glu	Ala	Asp	Pro	Thr	Asn	Pro	Ala	Leu	Arg	Glu	
		115					120					125				
GAG	ATG	CGC	ATT	CAA	TTC	AAT	GAC	ATG	AAC	AGC	GCC	CTG	ACC	ACC	GCT	432
Glu	Met	Arg	Ile	Gln	Phe	Asn	Asp	Met	Asn	Ser	Ala	Leu	Thr	Thr	Ala	
	130					135					140					
ATT	CCT	CTG	TTT	GCC	GTG	CAA	AAT	TAC	CAA	GTG	CCT	CTG	CTG	TCC	GTG	480
Ile	Pro	Leu	Phe	Ala	Val	Gln	Asn	Tyr	Gln	Val	Pro	Leu	Leu	Ser	Val	
145					150				155						160	
TAC	GTG	CAA	GCT	GCC	AAT	CTG	CAT	CTG	TCC	GTG	CTG	CGC	GAT	GTG	TCC	528
Tyr	Val	Gln	Ala	Ala	Asn	Leu	His	Leu	Ser	Val	Leu	Arg	Asp	Val	Ser	
			165					170					175			
GTG	TTT	GGC	CAA	AGG	TGG	GGC	TTT	GAT	GCC	GCC	ACC	ATC	AAT	AGC	CGC	576
Val	Phe	Gly	Gln	Arg	Trp	Gly	Phe	Asp	Ala	Ala	Thr	Ile	Asn	Ser	Arg	
		180					185						190			
TAC	AAT	GAT	CTG	ACC	AGG	CTG	ATT	GGC	AAC	TAC	ACC	GAT	TAC	GCT	GTG	624
Tyr	Asn	Asp	Leu	Thr	Arg	Leu	Ile	Gly	Asn	Tyr	Thr	Asp	Tyr	Ala	Val	
		195					200					205				
CGC	TGG	TAC	AAT	ACC	GGC	CTG	GAA	CGC	GTG	TGG	GGC	CCA	GAT	TCC	CGC	672

Arg 210	Trp	Tyr	Asn	Thr	Gly	Leu 215	Glu	Arg	Val	Trp	Gly 220	Pro	Asp	Ser	Arg	
GAT Asp 225	TGG Trp	GTG Val	AGG Arg	TAC Tyr	AAT Asn 230	CAA Gln	TTT Phe	CGC Arg	CGC Arg	GAA Glu 235	CTG Leu	ACC Thr	CTG Leu	ACC Thr	GTG Val 240	720
CTC Leu	GAT Asp	ATC Ile	GTG Val	GCT Ala 245	CTG Leu	TTC Phe	CCA Pro	AAT Asn	TAC Tyr 250	GAT Asp	AGC Ser	CGC Arg	CGC Arg	TAC Tyr 255	CCA Pro	768
ATT Ile	CGA Arg	ACC Thr	GTG Val 260	TCC Ser	CAA Gln	CTG Leu	ACC Thr	CGC Arg 265	GAA Glu	ATT Ile	TAC Tyr	ACC Thr	AAC Asn 270	CCA Pro	GTG Val	816
CTG Leu	GAA Glu	AAT Asn 275	TTT Phe	GAT Asp	GGT Gly	AGC Ser	TTT Phe 280	CGC Arg	GGC Gly	TCC Ser	GCT Ala	CAG Gln 285	GGC Gly	ATC Ile	GAA Glu	864
CGC Arg	AGC Ser 290	ATT Ile	AGG Arg	AGC Ser	CCA Pro	CAT His 295	CTG Leu	ATG Met	GAT Asp	ATC Ile	CTG Leu 300	AAC Asn	AGC Ser	ATC Ile	ACC Thr	912
ATC Ile 305	TAC Tyr	ACC Thr	GAT Asp	GCT Ala	CAT His 310	AGG Arg	GGT Gly	TAC Tyr	TAC Tyr	TAC Tyr 315	TGG Trp	TCC Ser	GGC Gly	CAT His	CAA Gln 320	960
ATC Ile	ATG Met	GCT Ala	TCC Ser 325	CCT Pro	GTG Val	GGC Gly	TTT Phe	TCC Ser	GGG Gly 330	CCA Pro	GAA Glu	TTC Phe	ACC Thr 335	TTT Phe	CCA Pro	1008
CTG Leu	TAC Tyr	GGC Gly 340	ACG Thr	ATG Met	GGC Gly	AAT Asn	GCC Ala 345	GCT Ala	CCA Pro	CAA Gln	CAA Gln	CGC Arg	ATT Ile 350	GTG Val	GCT Ala	1056
CAA Gln	CTG Leu	GGT Gly 355	CAG Gln	GGC Gly	GTG Val	TAC Tyr	CGC Arg 360	ACC Thr	CTG Leu	TCC Ser	TCC Ser	ACC Thr 365	CTG Leu	TAC Tyr	CGC Arg	1104
CGC Arg	CCT Pro 370	TTT Phe	AAT Asn	ATC Ile	GGC Gly	ATC Ile 375	AAC Asn	AAC Asn	CAG Gln	CAA Gln 380	CTG Leu	TCC Ser	GTG Val	CTG Leu	GAC Asp	1152
GGC Gly 385	ACC Thr	GAA Glu	TTT Phe	GCT Ala	TAC Tyr 390	GGC Gly	ACC Thr	TCC Ser	TCC Ser	AAT Asn 395	CTG Leu	CCA Pro	TCC Ser	GCT Ala	GTA Val 400	1200
TAC Tyr	CGC Arg	AAG Lys	AGC Ser	GGC Gly 405	ACC Thr	GTG Val	GAT Asp	TCC Ser	CTG Leu 410	GAT Asp	GAA Glu	ATC Ile	CCA Pro	CCA Pro 415	CAG Gln	1248
AAT Asn	AAC Asn	AAC Asn	GTG Val 420	CCA Pro	CCT Pro	AGG Arg	CAA Gln	GGC Gly 425	TTT Phe	AGC Ser	CAT His	CGC Arg	CTG Leu 430	AGC Ser	CAT His	1296
GTG Val	TCC Ser	ATG Met 435	TTT Phe	CGC Arg	TCC Ser	GGC Gly	TTT Phe 440	AGC Ser	AAT Asn	AGC Ser	AGC Ser	GTG Val 445	AGC Ser	ATC Ile	ATC Ile	1344
CGC	GCT	CCT	ATG	TTC	TCC	TGG	ATC	CAC	CGC	TCC	GCT	GAG	TTC	AAC	AAC	1392

[illegible]

Tyr	Thr	Pro	Ile	Asp	Ile	Ser	Leu	Ser	Leu	Thr	Gln	Phe	Leu	Leu	Ser	
		35					40					45				
Glu	Phe	Val	Pro	Gly	Ala	Gly	Phe	Val	Leu	Gly	Leu	Val	Asp	Ile	Ile	
	50					55					60					
Trp	Gly	Ile	Phe	Gly	Pro	Ser	Gln	Trp	Asp	Ala	Phe	Leu	Val	Gln	Ile	
65					70					75					80	
Glu	Gln	Leu	Ile	Asn	Gln	Arg	Ile	Glu	Glu	Phe	Ala	Arg	Asn	Gln	Ala	
				85					90					95		
Ile	Ser	Arg	Leu	Glu	Gly	Leu	Ser	Asn	Leu	Tyr	Gln	Ile	Tyr	Ala	Glu	
			100					105					110			
Ser	Phe	Arg	Glu	Trp	Glu	Ala	Asp	Pro	Thr	Asn	Pro	Ala	Leu	Arg	Glu	
		115					120					125				
Glu	Met	Arg	Ile	Gln	Phe	Asn	Asp	Met	Asn	Ser	Ala	Leu	Thr	Thr	Ala	
	130					135					140					
Ile	Pro	Leu	Phe	Ala	Val	Gln	Asn	Tyr	Gln	Val	Pro	Leu	Leu	Ser	Val	
145					150					155					160	
Tyr	Val	Gln	Ala	Ala	Asn	Leu	His	Leu	Ser	Val	Leu	Arg	Asp	Val	Ser	
				165					170					175		
Val	Phe	Gly	Gln	Arg	Trp	Gly	Phe	Asp	Ala	Ala	Thr	Ile	Asn	Ser	Arg	
			180					185					190			
Tyr	Asn	Asp	Leu	Thr	Arg	Leu	Ile	Gly	Asn	Tyr	Thr	Asp	Tyr	Ala	Val	
		195					200					205				
Arg	Trp	Tyr	Asn	Thr	Gly	Leu	Glu	Arg	Val	Trp	Gly	Pro	Asp	Ser	Arg	
	210					215					220					
Asp	Trp	Val	Arg	Tyr	Asn	Gln	Phe	Arg	Arg	Glu	Leu	Thr	Leu	Thr	Val	
225					230					235					240	
Leu	Asp	Ile	Val	Ala	Leu	Phe	Pro	Asn	Tyr	Asp	Ser	Arg	Arg	Tyr	Pro	
				245					250					255		
Ile	Arg	Thr	Val	Ser	Gln	Leu	Thr	Arg	Glu	Ile	Tyr	Thr	Asn	Pro	Val	
			260					265					270			
Leu	Glu	Asn	Phe	Asp	Gly	Ser	Phe	Arg	Gly	Ser	Ala	Gln	Gly	Ile	Glu	
		275					280					285				
Arg	Ser	Ile	Arg	Ser	Pro	His	Leu	Met	Asp	Ile	Leu	Asn	Ser	Ile	Thr	
	290					295					300					
Ile	Tyr	Thr	Asp	Ala	His	Arg	Gly	Tyr	Tyr	Tyr	Trp	Ser	Gly	His	Gln	
305					310					315					320	
Ile	Met	Ala	Ser	Pro	Val	Gly	Phe	Ser	Gly	Pro	Glu	Phe	Thr	Phe	Pro	
				325					330					335		
Leu	Tyr	Gly	Thr	Met	Gly	Asn	Ala	Ala	Pro	Gln	Gln	Arg	Ile	Val	Ala	
			340					345					350			

Gln	Leu	Gly	Gln	Gly	Val	Tyr	Arg	Thr	Leu	Ser	Ser	Thr	Leu	Tyr	Arg	
		355					360					365				
Arg	Pro	Phe	Asn	Ile	Gly	Ile	Asn	Asn	Gln	Gln	Leu	Ser	Val	Leu	Asp	
	370					375					380					
Gly	Thr	Glu	Phe	Ala	Tyr	Gly	Thr	Ser	Ser	Asn	Leu	Pro	Ser	Ala	Val	
385					390					395					400	
Tyr	Arg	Lys	Ser	Gly	Thr	Val	Asp	Ser	Leu	Asp	Glu	Ile	Pro	Pro	Gln	
				405					410					415		
Asn	Asn	Asn	Val	Pro	Pro	Arg	Gln	Gly	Phe	Ser	His	Arg	Leu	Ser	His	
			420					425					430			
Val	Ser	Met	Phe	Arg	Ser	Gly	Phe	Ser	Asn	Ser	Ser	Val	Ser	Ile	Ile	
		435					440					445				
Arg	Ala	Pro	Met	Phe	Ser	Trp	Ile	His	Arg	Ser	Ala	Glu	Phe	Asn	Asn	
	450					455					460					
Ile	Ile	Pro	Ser	Ser	Gln	Ile	Thr	Gln	Ile	Pro	Leu	Thr	Lys	Ser	Thr	
465					470					475					480	
Asn	Leu	Gly	Ser	Gly	Thr	Ser	Val	Val	Lys	Gly	Pro	Gly	Phe	Thr	Gly	
				485					490					495		
Gly	Asp	Ile	Leu	Arg	Arg	Thr	Ser	Pro	Gly	Gln	Ile	Ser	Thr	Leu	Arg	
			500					505					510			
Val	Asn	Ile	Thr	Ala	Pro	Leu	Ser	Gln	Arg	Tyr	Arg	Val	Arg	Ile	Arg	
		515					520					525				
Tyr	Ala	Ser	Thr	Thr	Asn	Leu	Gln	Phe	His	Thr	Ser	Ile	Asp	Gly	Arg	
	530					535					540					
Pro	Ile	Asn	Gln	Gly	Asn	Phe	Ser	Ala	Thr	Met	Ser	Ser	Gly	Ser	Asn	
545					550					555					560	
Leu	Gln	Ser	Gly	Ser	Phe	Arg	Thr	Val	Gly	Phe	Thr	Thr	Pro	Phe	Asn	
				565					570					575		
Phe	Ser	Asn	Gly	Ser	Ser	Val	Phe	Thr	Leu	Ser	Ala	His	Val	Phe	Asn	
			580					585					590			
Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe	Val	Pro	Ala	Glu	
		595					600					605				
Val	Thr	Phe	Glu	Leu	Glu											

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Ile Thr Phe Thr Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCTTGGCAGC CATCACGTTC ACGGGAAGTA TTGTC 35

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 45 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATCTGGCAGC AGAAAAACAA GTAGTTGAGA ACTAAGAAGA AGAAA 45

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CATCGAGACA AGCACGGTCA ACTTC 25

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AAGTCCCTGG AGGCACAGGG CTTCAAGA 28



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AGCTTGCAGC GAGTACATAC ATACTAGGCA GCCAGGCAGC CATGGCGCCC ACCGTGATGA	60
TGGCCTCGTC GGCCACCGCC GTCGCTCCGT TCCAGGGGCT CAAGTCCACC GCCAGCCTCC	120
CCGTCGCCCCG CCGGTCCTCC AGAAGCCTCG GCAACGTCAG CAACGGCGGA AGGATCCGGT	180
GCATG	185

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ACGTCGCTCA TGTATGTATG ATCCGTCGGT CCGTCGGTAC CGCGGGTGGC ACTACTACCG	60
GAGCAGCCGG TGGCGGCAGC GAGGCAAGGT CCCCAGAGTTC AGGTGGCGGT CGGAGGGGCA	120
GCGGGCGGCC AGGAGGTCTT CGGAGCCGTT GCAGTCGTTG CCGCCTTCCT AGGCCAC	177

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATCACTTTCA CGGGA	15
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(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATCACGTTCA CGGCA	15
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(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GCTTACCTAC TAATTGTTCT TGG

23

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CAGGGTACAT ATTTGCCTTG GG

22

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AACCCTGAAT GGAAGTGC

18

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ACGGACAGAT GCAGATTGG

19